

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lee, Se-Jin
Huynh, Thanh
- (ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-5
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson, P.C.
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037
-
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows95
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/455,559
(B) FILING DATE: 31-MAY-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/003,144
(B) FILING DATE: 12-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lisa A. Haile, Ph.D.
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 07265/057001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619/678-5070
(B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCG GNTGGGARMG NTGGRTNR

28

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 121

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1..42

(C) OTHER INFORMATION: / N at residue 13, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCT CANCCRCAYT CRTCNACNAC CATRTCCTCR TA

42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(ix) FEATURE:

(B) LOCATION: 1..7

(C) OTHER INFORMATION: Xaa at residue 4 = Arg or Ser; Xaa at residue 6 and 7 = Val, Ile or Met

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Trp Glu Xaa Trp Xaa Xaa

1

5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 141

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1..35
- (C) OTHER INFORMATION: N at residue 12, 27, 30 and 33 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGAATTCG GNTGGVANRA YTGGR TNRTN KCNCC

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 145

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1..33
- (C) OTHER INFORMATION: N at residue 13, 19, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCTR CANSRCRANG MNTCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 141

(ix) FEATURE:

- (B) LOCATION: 1..9
- (C) OTHER INFORMATION: Xaa at residue 3 = His, Gln, Asn, Lys, Glu or Asp; Xaa at residue 4 = Asp or Asn; Xaa at residues 6 and 7 = Val, Ile or Met; Xaa at residue 8 = Glu or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 145

(ix) FEATURE:

- (B) LOCATION: 1..8
- (C) OTHER INFORMATION: Xaa at residues 2 and 3 = Val, Ile, Met, Thr or Ala; Xaa at residue 4 = Asp or Glu; Xaa at residue 5 = Ala or Ser; Xaa at residue 7 = Gly, Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe Pro, Ser, Thr, Trp, Tyr, and Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Xaa Xaa Xaa Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GD-5

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 322...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCAAGCCCT	CAGTCAGTTG	TGCGGGAGAA	AGGGGGCGGT	CGGCTTTCTC	CTTTCAAGAA	60
CGAGTTATTT	TCAGCTGCTG	ACTGGAGACG	GTGCACGTCT	GGACACGGGA	GCACTTCCAC	120
TATGGGACTG	GATACAGACA	CACGCCCGGC	GGACTTCAAG	ACACTCAGAC	TGAGGAGAAA	180
GCCCTGCCTG	CTGCTGCTGC	TGCTGCTGCT	GCCACCGCTG	CCTCTGAAGA	CCCACTCCTT	240
TCATGGTTTT	TCCTGCCAAG	CCAGAGGCAC	CTTCGCTGCT	ACGGCCTTTC	TCTGTGGTGT	300
CATTGAGCGG	CTGGCCAGAG	G ATG AGA CTC CCC AAA	CTC CTC ACT CTT TTG			351
		Met Arg Leu Pro Lys	Leu Leu Thr Leu Leu			
		1 5 10				
CTG TGG CAC CTG GCT TGG CTG GAC CTG GAA CTC ATC TGC ACT GTG CTG						399
Leu Trp His Leu Ala Trp Leu Asp Leu Glu Leu Ile Cys Thr Val Leu						
	15	20	25			
GGT GCC CCT GAC TTA GGA CAG AGA ACC CCA GGG GCC AAG CCA GGG TTG						447
Gly Ala Pro Asp Leu Gly Gln Arg Thr Pro Gly Ala Lys Pro Gly Leu						
	30	35	40			
ACC AAA GCG GAG GCC AAG GAG AGG CCA CCC CTG GCC AGG AAT GTC TTT						495
Thr Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu Ala Arg Asn Val Phe						
	45	50	55			
AGG CCA GGG GGT CAT ATC TAT GGT GTG GGG GCC ACC AAT GCC AGG GCC						543
Arg Pro Gly Gly His Ile Tyr Gly Val Gly Ala Thr Asn Ala Arg Ala						
	60	65	70			
AAG GGA AGC TCT GGG CAG ACA CAG GCC AAG AAG GAT GAA CCC AGA AAG						591
Lys Gly Ser Ser Gly Gln Thr Gln Ala Lys Lys Asp Glu Pro Arg Lys						
	75	80	85	90		
ATG CCC CCC AGA TCC GGT GGC TCT GAA ACC AAG CCA GGA CCC TCT TCC						639

Met	Pro	Pro	Arg	Ser	Gly	Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Ser		
				95					100					105			
CAG	ACT	AGA	CAG	GCT	GCA	GCC	CGG	ACT	GTA	ACC	CCA	AAA	GGA	CAG	CTT	687	
Gln	Thr	Arg	Gln	Ala	Ala	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu		
			110					115					120				
CCT	GGG	GGC	AAA	GCA	TCT	TCA	AAA	GCA	GGA	TCT	GCC	CCC	AGC	TCC	TTC	735	
Pro	Gly	Gly	Lys	Ala	Ser	Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe		
			125				130					135					
CTG	CTG	AAG	AAG	ACC	AGG	GAG	CCT	GGG	ACC	CCT	CGA	GAG	CCC	AAG	GAG	783	
Leu	Leu	Lys	Lys	Thr	Arg	Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu		
			140			145					150						
CCG	TTC	CGC	CCG	CCC	CCC	ATC	ACA	CCC	CAC	GAA	TAC	ATG	CTC	TCC	CTG	831	
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu		
					160					165					170		
TAC	AGG	ACG	CTG	TCC	GAT	GCT	GAC	AGA	AAG	GGA	GGT	AAC	AGC	AGC	GTG	879	
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val		
				175					180					185			
AAG	TTG	GAG	GCT	GGC	CTG	GCC	AAC	ACC	ATC	ACC	AGC	TTT	ATT	GAC	AAA	927	
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys		
			190					195					200				
GGG	CAA	GAT	GAC	CGA	GGC	CCT	GCG	GTC	AGG	AAG	CAG	AGG	TAC	GTG	TTT	975	
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe		
		205					210					215					
GAC	ATC	AGT	GCC	TTG	GAG	AAG	GAT	GGG	CTG	TTG	GGG	GCT	GAA	CTG	CGG	1023	
Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg		
			220			225					230						
ATC	TTA	CGG	AAG	AAG	CCC	TTG	GAC	GTG	GCC	AAG	CCA	GCG	GTC	CCC	AGT	1071	
Ile	Leu	Arg	Lys	Lys	Pro	Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser		
					240					245					250		
AGC	GGG	CGG	GTT	GCC	CAA	CTG	AAG	CTG	TCC	AGC	TGC	CCC	AGC	GGC	CGG	1119	
Ser	Gly	Arg	Val	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg		
				255				260						265			
CAG	CCG	GCA	GCC	TTG	CTG	GAT	GTG	CGC	TCC	GTG	CCA	GGC	CTG	GAT	GGA	1167	
Gln	Pro	Ala	Ala	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly		
			270					275					280				
TCT	GGC	TGG	GAG	GTG	TTC	GAC	ATC	TGG	AAG	CTC	TTC	CGA	AAT	TTT	AAG	1215	
Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys		
			285				290					295					
AAC	TCA	GCG	CAG	CTG	TGC	CTG	GAG	CTG	GAG	GCC	TGG	GAA	CGG	GGC	CGG	1263	
Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg		
			300			305					310						

GCC GTG GAC CTC CGT GGC CTG GGC TTT GAA CGC ACT GCC CGA CAG GTC 1311
 Ala Val Asp Leu Arg Gly Leu Gly Phe Glu Arg Thr Ala Arg Gln Val
 315 320 325 330

CAC GAG AAA GCC TTG TTC CTA GTG TTT GGT CGT ACC AAG AAA CGG GAC 1359
 His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp
 335 340 345

CTG TTC TTT AAT GAG ATT AAG GCC CGC TCT GGC CAG GAT GAC AAG ACT 1407
 Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr
 350 355 360

GTG TAT GAA TAT TTG TTC AGC CAG CGG CGG AAA CGC CGG GCC CCA TTG 1455
 Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu
 365 370 375

GCC AAT CGC CAG GGC AAG CGA CCC AGC AAG AAC CTC AAG GCT CGC TGC 1503
 Ala Asn Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
 380 385 390

AGT CGC AAG GCC TTG CAT GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC 1551
 Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp
 395 400 405 410

TGG ATC ATC GCA CCT CTT GAG TAT GAG GCC TTC CAC TGC GAA GGA CTG 1599
 Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu
 415 420 425

TGT GAG TTC CCC TTG CGC TCC CAC TTG GAG CCC ACA AAC CAC GCA GTC 1647
 Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val
 430 435 440

ATT CAG ACC CTA ATG AAC TCT ATG GAC CCT GAA TCC ACA CCA CCC ACT 1695
 Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr
 445 450 455

TGT TGT GTG CCT ACA CGG CTG AGT CCT ATT AGC ATC CTC TTC ATC GAC 1743
 Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp
 460 465 470

TCT GCC AAC AAC GTG GTG TAT AAA CAG TAC GAG GAC ATG GTC GTG GAA 1791
 Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu
 475 480 485 490

TCT TGT GGC TGC AGG TAGCAGCACC GGCCACCTG TCTTCCAGGG TGGCACATCC A 1847
 Ser Cys Gly Cys Arg
 495

GAGACTACCC CCTCTACAGG TTCCTGGAGT AACAGAGAGC CTGTGAAGCT GCTGCCCCGAA 1907
 GTTTCCTGGC AGCCTGCAGG AAAGAGTTCT CAGCAGGCTT ACTCTCTGGA TGTGATCTGG 1967
 ACTAAAGAGA TCACCTTCTG AAGATTCTCTG CCCAAGGAAC AGACTCTGAG TGGGCCTGGG 2027
 GCTCAGGAAA GGTGTTCTTA ATGAGATTCA GTTCACCATC TCTCCTGCCG GGGCCGAGAA 2087
 CCTTCATTTT TCTCCAGACT CTCCAGAGAA GTTGTAGCTA TATCCTAAGC TCTTTAAGGG 2147
 AGAGCTGTCT CCTCCTTGAA TCACCTTTGT GCCTGGTGAC TTTCTGCCAC GAGATGTTCA 2207
 TTACAGGGGC TGGGCAAAGA AGGGGAAAGG GCTTGGGCAG GGGTGAAGAG AAGAGTATGA 2267

GCCTAATTAG ACTGTTAGAT TAAAATGTAC ATCGATGACA TAAAAGCTGA ATCTTCATGG 2327
CT 2329

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Arg	Leu	Pro	Lys	Leu	Leu	Thr	Leu	Leu	Leu	Trp	His	Leu	Ala	Trp
1				5				10						15	
Leu	Asp	Leu	Glu	Leu	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
			20					25					30		
Gln	Arg	Thr	Pro	Gly	Ala	Lys	Pro	Gly	Leu	Thr	Lys	Ala	Glu	Ala	Lys
			35					40					45		
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ile
	50					55				60					
Tyr	Gly	Val	Gly	Ala	Thr	Asn	Ala	Arg	Ala	Lys	Gly	Ser	Ser	Gly	Gln
65					70					75					80
Thr	Gln	Ala	Lys	Lys	Asp	Glu	Pro	Arg	Lys	Met	Pro	Pro	Arg	Ser	Gly
				85				90					95		
Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Ser	Gln	Thr	Arg	Gln	Ala	Ala
			100					105					110		
Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu	Pro	Gly	Gly	Lys	Ala	Ser
	115						120					125			
Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe	Leu	Leu	Lys	Lys	Thr	Arg
	130					135				140					
Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu	Pro	Phe	Arg	Pro	Pro	Pro
145					150					155					160
Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu	Tyr	Arg	Thr	Leu	Ser	Asp
				165					170					175	
Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val	Lys	Leu	Glu	Ala	Gly	Leu
			180					185					190		
Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys	Gly	Gln	Asp	Asp	Arg	Gly
	195						200					205			
Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	Asp	Ile	Ser	Ala	Leu	Glu
	210					215					220				
Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	Ile	Leu	Arg	Lys	Lys	Pro
225					230					235					240
Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser	Ser	Gly	Arg	Val	Ala	Gln
				245					250					255	
Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg	Gln	Pro	Ala	Ala	Leu	Leu
			260					265					270		
Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	Ser	Gly	Trp	Glu	Val	Phe
	275						280					285			
Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	Asn	Ser	Ala	Gln	Leu	Cys

290		295		300												
Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg	Ala	Val	Asp	Leu	Arg	Gly	
305		310		315		320		325		330		335		340		345
Leu	Gly	Phe	Glu	Arg	Thr	Ala	Arg	Gln	Val	His	Glu	Lys	Ala	Leu	Phe	
Leu	Val	Phe	Gly	Arg	Thr	Lys	Lys	Arg	Asp	Leu	Phe	Phe	Asn	Glu	Ile	
Lys	Ala	Arg	Ser	Gly	Gln	Asp	Asp	Lys	Thr	Val	Tyr	Glu	Tyr	Leu	Phe	
Ser	Gln	Arg	Arg	Lys	Arg	Arg	Ala	Pro	Leu	Ala	Asn	Arg	Gln	Gly	Lys	
370		375		380		385		390		395		400		405		
Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala	Arg	Cys	Ser	Arg	Lys	Ala	Leu	His	
Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu	
Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	Gly	Leu	Cys	Glu	Phe	Pro	Leu	Arg	
Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Val	Ile	Gln	Thr	Leu	Met	Asn	
435		440		445		450		455		460		465		470		
Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro	Thr	Cys	Cys	Val	Pro	Thr	Arg	
Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	Ile	Asp	Ser	Ala	Asn	Asn	Val	Val	
465		470		475		480		485		490		495		499		
Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg	Leu	Arg	Arg	His	Thr	Glu	Pro	Arg	Val	Glu	Val	Gly	Pro	Val	Gly
1				5					10					15	
Thr	Cys	Arg	Thr	Arg	Arg	Leu	His	Val	Ser	Phe	Arg	Glu	Val	Gly	Trp
				20				25					30		
His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Phe	Cys	Gln
				35			40					45			
Gly	Thr	Cys	Ala	Leu	Pro	Glu	Thr	Leu	Arg	Gly	Pro	Gly	Gly	Pro	Pro
				50			55				60				
Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro
65				70					75					80	
Thr	Pro	Gly	Ala	Gly	Ser	Pro	Cys	Cys	Val	Pro	Glu	Arg	Leu	Ser	Pro
				85				90					95		
Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Glu	Asp	Asn	Val	Val	Leu	Arg	His

100 105 110
 Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg	Lys	Arg	Arg	Ala	Ala	Ile	Ser	Val	Pro	Lys	Gly	Phe	Cys	Arg	Asn
1				5					10					15	
Phe	Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp
			20					25					30		
His	Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His
		35					40					45			
Gly	Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr
	50					55					60				
Ala	Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys
65				70						75					80
Ala	Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln
			85						90					95	
Asp	Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val
			100					105					110		
Asp	Glu	Cys	Gly	Cys	Gly										
			115												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro	Leu	Ala	Asn	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala
1				5					10					15	
Arg	Cys	Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
1 5 10 15
Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
20 25 30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
35 40 45
Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
65 70 75 80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
85 90 95
Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
100 105 110
Glu Gly Cys Gly Cys Arg
115

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
1 5 10 15
Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
20 25 30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
35 40 45
Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
65 70 75 80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
85 90 95
Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
100 105 110
Glu Gly Cys Gly Cys Arg

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vgr-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser	Arg	Gly	Ser	Gly	Ser	Ser	Asp	Tyr	Asn	Gly	Ser	Glu	Leu	Lys	Thr
1				5					10					15	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp
			20					25					30		
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp
		35					40					45			
Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His
	50					55					60				
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro
65					70					75					80
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr
				85					90					95	
Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val
			100					105					110		
Val	Arg	Ala	Cys	Gly	Cys	His									
															115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
1				5					10					15	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp
			20					25					30		
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu

	35					40						45							
Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His				
	50					55					60								
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro				
	65					70				75					80				
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr				
				85					90					95					
Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val				
			100					105					110						
Val	Arg	Ala	Cys	Gly	Cys	His													
			115																

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BMP-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser	Arg	Met	Ser	Ser	Val	Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln				
1				5					10					15					
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp				
			20				25						30						
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp				
		35				40					45								
Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His				
	50					55					60								
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro				
	65				70					75					80				
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr				
				85					90					95					
Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val				
			100					105					110						
Val	Arg	Ser	Cys	Gly	Cys	His													
			115																

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
1 5 10 15
Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
20 25 30
Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
35 40 45
Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
50 55 60
Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
65 70 75 80
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
85 90 95
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
100 105 110
Thr Val Glu Ser Cys Ala Cys Arg
115 120

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: MIS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
1 5 10 15
Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
20 25 30
Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
35 40 45
Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
50 55 60
Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
65 70 75 80
Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
85 90 95
Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
100 105 110
Cys Gly Cys Arg
115

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala	Leu	Arg	Leu	Leu	Gln	Arg	Pro	Pro	Glu	Glu	Pro	Ala	Ala	His	Ala	
1				5					10					15		
Asn	Cys	His	Arg	Val	Ala	Leu	Asn	Ile	Ser	Phe	Gln	Glu	Leu	Gly	Trp	
			20					25					30			
Glu	Arg	Trp	Ile	Val	Tyr	Pro	Pro	Ser	Phe	Ile	Phe	His	Tyr	Cys	His	
		35					40					45				
Gly	Gly	Cys	Gly	Leu	His	Ile	Pro	Pro	Asn	Leu	Ser	Leu	Pro	Val	Pro	
	50					55					60					
Gly	Ala	Pro	Pro	Thr	Pro	Ala	Gln	Pro	Tyr	Ser	Leu	Leu	Pro	Gly	Ala	
65					70					75					80	
Gln	Pro	Cys	Cys	Ala	Ala	Leu	Pro	Gly	Thr	Met	Arg	Pro	Leu	His	Val	
			85						90					95		
Arg	Thr	Thr	Ser	Asp	Gly	Gly	Tyr	Ser	Phe	Lys	Tyr	Glu	Thr	Val	Pro	
			100					105					110			
Asn	Leu	Leu	Thr	Gln	His	Cys	Ala	Cys	Ile							
			115				120									

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His	Arg	Arg	Arg	Arg	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Lys	Val	Asn	Ile	
1				5					10					15		
Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn	
			20					25					30			
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly	
		35					40					45				
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe	
	50					55					60					

His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe
65					70					75					80
Ala	Asn	Leu	Lys	Ser	Cys	Cys	Val	Pro	Thr	Lys	Leu	Arg	Pro	Met	Ser
				85					90					95	
Met	Leu	Tyr	Tyr	Asp	Asp	Gly	Gln	Asn	Ile	Ile	Lys	Lys	Asp	Ile	Gln
			100					105					110		
Asn	Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ser						
		115					120								

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His	Arg	Ile	Arg	Lys	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Arg	Thr	Asn	Leu
1				5					10					15	
Cys	Cys	Arg	Gln	Gln	Phe	Phe	Ile	Asp	Phe	Arg	Leu	Ile	Gly	Trp	Asn
			20					25					30		
Asp	Trp	Ile	Ile	Ala	Pro	Thr	Gly	Tyr	Tyr	Gly	Asn	Tyr	Cys	Glu	Gly
		35					40					45			
Ser	Cys	Pro	Ala	Tyr	Leu	Ala	Gly	Val	Pro	Gly	Ser	Ala	Ser	Ser	Phe
	50					55				60					
His	Thr	Ala	Val	Val	Asn	Gln	Tyr	Arg	Met	Arg	Gly	Leu	Asn	Pro	Gly
65					70					75					80
Thr	Val	Asn	Ser	Cys	Cys	Ile	Pro	Thr	Lys	Leu	Ser	Thr	Met	Ser	Met
				85					90					95	
Leu	Tyr	Phe	Asp	Asp	Glu	Tyr	Asn	Ile	Val	Lys	Arg	Asp	Val	Pro	Asn
			100					105					110		
Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ala							
		115					120								

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
1 5 10 15
Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
20 25 30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
35 40 45
Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
50 55 60
Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
65 70 75 80
Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
85 90 95
Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
100 105 110
Lys Cys Ser
115

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
1 5 10 15
Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
20 25 30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
35 40 45
Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
50 55 60
Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
65 70 75 80
Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
85 90 95
Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
100 105 110
Lys Cys Ser
115

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu
1 5 10 15
Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly
20 25 30
Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser
35 40 45
Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val
50 55 60
Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys
65 70 75 80
~~Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly~~
85 90 95
Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys
100 105 110
Lys Cys Ser
115

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lee, Se-Jin
Huynh, Thanh
- (ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-5
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Fish & Richardson, P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
-
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/455,559
 - (B) FILING DATE: 31-MAY-1995
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/003,144
 - (B) FILING DATE: 12-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Lisa A. Haile, Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07265/057001
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCTG GNTGGGARMG NTGGRTNR

28

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 121

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1..42

(C) OTHER INFORMATION: / N at residue 13, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCTR CANCCRCAYT CRTCNACNAC CATRTCYTCR TA

42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(ix) FEATURE:

(B) LOCATION: 1..7

(C) OTHER INFORMATION: Xaa at residue 4 = Arg or Ser; Xaa at residue 6 and 7 = Val, Ile or Met

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Trp Glu Xaa Trp Xaa Xaa

1

5

-

[illegible][illegible]

- | | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298 | 2299 | 2300 | 2301 | 2302 | 2303 | 2304 | 2305 | 2306 | 2307 | 2308 | 2309 | 2310 | 2311 | 2312 | 2313 | 2314 | 2315 | 2316 | 2317 | 2318 | 2319 | 2320 | 2321 | 2322 | 2323 | 2324 | 2325 | 2326 | 2327 | 2328 | 2329 | 2330 | 2331 | 2332 | 2333 | 2334 | 2335 | 2336 | 2337 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | 2347 | 2348 | 2349 | 2350 | 2351 | 2352 | 2353 | 2354 | 2355 | 2356 | 2357 | 2358 | 2359 | 2360 | 2361 | 2362 | 2363 | 2364 | 2365 | 2366 | 2367 | 2368 | 2369 | 2370 | 2371 | 2372 | 2373 | 2374 | 2375 | 2376 | 2377 | 2378 | 2379 | 2380 | 2381 | 2382 | 2383 | 2384 | 2385 | 2386 | 2387 | 2388 | 2389 | 2390 | 2391 | 2392 | 2393 | 2394 | 2395 | 2396 | 2397 | 2398 | 2399 | 2400 | 2401 | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 | 2408 | 2409 | 2410 | 2411 | 2412 | 2413 | 2414 | 2415 | 2416 | 2417 | 2418 | 2419 | 2420 | 2421 | 2422 | 2423 | 2424 | 2425 | 2426 | 2427 | 2428 | 2429 | 2430 | 2431 | 2432 | 2 |
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|

35

35

- 35

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1..33
- (C) OTHER INFORMATION: N at residue 13, 19, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCTCANSRCRCANGMNTCNACNRYCAT

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 141

(ix) FEATURE:

- (B) LOCATION: 1..9
- (C) OTHER INFORMATION: Xaa at residue 3 = His, Gln, Asn, Lys, Glu or Asp; Xaa at residue 4 = Asp or Asn; Xaa at residues 6 and 7 = Val, Ile or Met; Xaa at residue 8 = Glu or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 145

(ix) FEATURE:

- (B) LOCATION: 1..8
- (C) OTHER INFORMATION: Xaa at residues 2 and 3 = Val, Ile, Met, Thr or Ala; Xaa at residue 4 = Asp or Glu; Xaa at residue 5 = Ala or Ser; Xaa at residue 7 = Gly, Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe Pro, Ser, Thr, Trp, Tyr, and Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Xaa Xaa Xaa Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: GD-5

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 322...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCAAGCCCT CAGTCAGTTG TGCGGGAGAA AGGGGGCGGT CGGCTTTCTC CTTTCAAGAA	60
CGAGTTATTT TCAGCTGCTG ACTGGAGACG GTGCACGTCT GGACACGGGA GCACTTCCAC	120
TATGGGACTG GATACAGACA CACGCCCGGC GGACTTCAAG ACACTCAGAC TGAGGAGAAA	180
GCCCTGCCTG CTGCTGCTGC TGCTGCTGCT GCCACCGCTG CCTCTGAAGA CCCACTCCTT	240
TCATGGTTTT TCCTGCCAAG CCAGAGGCAC CTTGCTGCT ACGGCCTTTC TCTGTGGTGT	300
CATTCAGCGG CTGGCCAGAG G ATG AGA CTC CCC AAA CTC CTC ACT CTT TTG	351
Met Arg Leu Pro Lys Leu Leu Thr Leu Leu	
1 5 10	
CTG TGG CAC CTG GCT TGG CTG GAC CTG GAA CTC ATC TGC ACT GTG CTG	399
Leu Trp His Leu Ala Trp Leu Asp Leu Glu Leu Ile Cys Thr Val Leu	
15 20 25	
GGT GCC CCT GAC TTA GGA CAG AGA ACC CCA GGG GCC AAG CCA GGG TTG	447
Gly Ala Pro Asp Leu Gly Gln Arg Thr Pro Gly Ala Lys Pro Gly Leu	
30 35 40	
ACC AAA GCG GAG GCC AAG GAG AGG CCA CCC CTG GCC AGG AAT GTC TTT	495
Thr Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu Ala Arg Asn Val Phe	
45 50 55	
AGG CCA GGG GGT CAT ATC TAT GGT GTG GGG GCC ACC AAT GCC AGG GCC	543
Arg Pro Gly Gly His Ile Tyr Gly Val Gly Ala Thr Asn Ala Arg Ala	
60 65 70	
AAG GGA AGC TCT GGG CAG ACA CAG GCC AAG AAG GAT GAA CCC AGA AAG	591
Lys Gly Ser Ser Gly Gln Thr Gln Ala Lys Lys Asp Glu Pro Arg Lys	
75 80 85 90	
ATG CCC CCC AGA TCC GGT GGC TCT GAA ACC AAG CCA GGA CCC TCT TCC	639

Met	Pro	Pro	Arg	Ser	Gly	Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Ser	
				95					100					105		
CAG	ACT	AGA	CAG	GCT	GCA	GCC	CGG	ACT	GTA	ACC	CCA	AAA	GGA	CAG	CTT	687
Gln	Thr	Arg	Gln	Ala	Ala	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu	
			110					115					120			
CCT	GGG	GGC	AAA	GCA	TCT	TCA	AAA	GCA	GGA	TCT	GCC	CCC	AGC	TCC	TTC	735
Pro	Gly	Gly	Lys	Ala	Ser	Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe	
			125				130					135				
CTG	CTG	AAG	AAG	ACC	AGG	GAG	CCT	GGG	ACC	CCT	CGA	GAG	CCC	AAG	GAG	783
Leu	Leu	Lys	Lys	Thr	Arg	Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu	
			140			145					150					
CCG	TTC	CGC	CCG	CCC	CCC	ATC	ACA	CCC	CAC	GAA	TAC	ATG	CTC	TCC	CTG	831
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu	
					160					165					170	
TAC	AGG	ACG	CTG	TCC	GAT	GCT	GAC	AGA	AAG	GGA	GGT	AAC	AGC	AGC	GTG	879
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val	
				175					180					185		
AAG	TTG	GAG	GCT	GGC	CTG	GCC	AAC	ACC	ATC	ACC	AGC	TTT	ATT	GAC	AAA	927
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys	
			190					195					200			
GGG	CAA	GAT	GAC	CGA	GGC	CCT	GCG	GTC	AGG	AAG	CAG	AGG	TAC	GTG	TTT	975
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	
		205					210					215				
GAC	ATC	AGT	GCC	TTG	GAG	AAG	GAT	GGG	CTG	TTG	GGG	GCT	GAA	CTG	CGG	1023
Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	
		220				225					230					
ATC	TTA	CGG	AAG	AAG	CCC	TTG	GAC	GTG	GCC	AAG	CCA	GCG	GTC	CCC	AGT	1071
Ile	Leu	Arg	Lys	Lys	Pro	Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser	
					240					245					250	
AGC	GGG	CGG	GTT	GCC	CAA	CTG	AAG	CTG	TCC	AGC	TGC	CCC	AGC	GGC	CGG	1119
Ser	Gly	Arg	Val	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg	
				255					260					265		
CAG	CCG	GCA	GCC	TTG	CTG	GAT	GTG	CGC	TCC	GTG	CCA	GGC	CTG	GAT	GGA	1167
Gln	Pro	Ala	Ala	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	
			270					275					280			
TCT	GGC	TGG	GAG	GTG	TTC	GAC	ATC	TGG	AAG	CTC	TTC	CGA	AAT	TTT	AAG	1215
Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	
		285					290					295				
AAC	TCA	GCG	CAG	CTG	TGC	CTG	GAG	CTG	GAG	GCC	TGG	GAA	CGG	GGC	CGG	1263
Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg	
		300				305					310					

GAGACTACCC	CCTCTACAGG	TTCCTGGAGT	AACAGAGAGC	CTGTGAAGCT	GCTGCCCGAA	1907
GTTTCCTGGC	AGCCTGCAGG	AAAGAGTTCT	CAGCAGGCTT	ACTCTCTGGA	TGTGATCTGG	1967
ACTAAAGAGA	TCACCTTCTG	AAGATTCTCG	CCCAAGGAAC	AGACTCTGAG	TGGGCCTGGG	2027
GCTCAGGAAA	GGTGTTCCTTA	ATGAGATTCA	GTTCCACCATC	TCTCCTGCCG	GGGCCGGAGA	2087
CCTTCATTTC	TCTCCAGACT	CTCCAGAGAA	GTTGTAGCTA	TATCCTAAGC	TCTTTAAGGG	2147
AGAGCTGTCT	CCTCCTTGAA	TCACCTTTGT	GCCTGGTGAC	TTTCTGCCAC	GAGATGTTCA	2207
TTACAGGGGC	TGGGCAAAGA	AGGGGAAAGG	GCTTGGGCAG	GGGTGAAGAG	AAGAGTATGA	2267

GCCTAATTAG ACTGTTAGAT TAAAATGTAC ATCGATGACA TAAAAGCTGA ATCTTCATGG 2327
CT 2329

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Arg	Leu	Pro	Lys	Leu	Leu	Thr	Leu	Leu	Leu	Trp	His	Leu	Ala	Trp
1				5					10					15	
Leu	Asp	Leu	Glu	Leu	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
			20					25					30		
Gln	Arg	Thr	Pro	Gly	Ala	Lys	Pro	Gly	Leu	Thr	Lys	Ala	Glu	Ala	Lys
			35					40					45		
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ile
	50					55					60				
Tyr	Gly	Val	Gly	Ala	Thr	Asn	Ala	Arg	Ala	Lys	Gly	Ser	Ser	Gly	Gln
65					70					75					80
Thr	Gln	Ala	Lys	Lys	Asp	Glu	Pro	Arg	Lys	Met	Pro	Pro	Arg	Ser	Gly
				85					90					95	
Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Ser	Gln	Thr	Arg	Gln	Ala	Ala
			100					105					110		
Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu	Pro	Gly	Gly	Lys	Ala	Ser
			115				120						125		
Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe	Leu	Leu	Lys	Lys	Thr	Arg
			130				135					140			
Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu	Pro	Phe	Arg	Pro	Pro	Pro
145					150					155					160
Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu	Tyr	Arg	Thr	Leu	Ser	Asp
				165					170					175	
Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val	Lys	Leu	Glu	Ala	Gly	Leu
			180					185					190		
Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys	Gly	Gln	Asp	Asp	Arg	Gly
			195				200					205			
Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	Asp	Ile	Ser	Ala	Leu	Glu
			210				215					220			
Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	Ile	Leu	Arg	Lys	Lys	Pro
225					230					235					240
Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser	Ser	Gly	Arg	Val	Ala	Gln
				245					250					255	
Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg	Gln	Pro	Ala	Ala	Leu	Leu
			260					265					270		
Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	Ser	Gly	Trp	Glu	Val	Phe
			275				280					285			
Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	Asn	Ser	Ala	Gln	Leu	Cys

290		295		300
Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg Ala Val Asp Leu Arg Gly				
305		310		315
Leu Gly Phe Glu Arg Thr Ala Arg Gln Val His Glu Lys Ala Leu Phe				
	325		330	
Leu Val Phe Gly Arg Thr Lys Lys Arg Asp Leu Phe Phe Asn Glu Ile				
	340		345	
Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr Val Tyr Glu Tyr Leu Phe				
	355		360	
Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu Ala Asn Arg Gln Gly Lys				
	370		375	
Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His				
385		390		395
Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile Ile Ala Pro Leu				
	405		410	
Glu Tyr Glu Ala Phe His Cys Glu Gly Leu Cys Glu Phe Pro Leu Arg				
	420		425	
Ser His Leu Glu Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn				
	435		440	
Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys Val Pro Thr Arg				
	450		455	
Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp Ser Ala Asn Asn Val Val				
465		470		475
Tyr Lys Gln Tyr Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg				
	485		490	
				495

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: **protein**

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Leu Arg Arg His Thr Glu Pro Arg Val Glu Val Gly Pro Val Gly	
1	5
Thr Cys Arg Thr Arg Arg Leu His Val Ser Phe Arg Glu Val Gly Trp	
	20
His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Phe Cys Gln	
	35
Gly Thr Cys Ala Leu Pro Glu Thr Leu Arg Gly Pro Gly Gly Pro Pro	
	50
Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro	
	65
Thr Pro Gly Ala Gly Ser Pro Cys Cys Val Pro Glu Arg Leu Ser Pro	
	85
Ile Ser Val Leu Phe Phe Asp Asn Glu Asp Asn Val Val Leu Arg His	

100 105 110
 Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg	Lys	Arg	Arg	Ala	Ala	Ile	Ser	Val	Pro	Lys	Gly	Phe	Cys	Arg	Asn
1				5					10					15	
Phe	Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp
			20					25					30		
His	Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His
		35					40					45			
Gly	Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr
	50					55					60				
Ala	Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys
	65				70					75					80
Ala	Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln
			85					90						95	
Asp	Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val
			100					105					110		
Asp	Glu	Cys	Gly	Cys	Gly										
			115												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro	Leu	Ala	Asn	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala
1				5					10					15	
Arg	Cys	Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Smoking status	
Current smoker	18.7%
Former smoker	25.3%
Non-smoker	56.0%
Alcohol consumption	
Regular	15.2%
Occasional	22.8%
Never	62.0%

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(B) CLONE: GDF-9

(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
 1           5           10           15
Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
           20           25           30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
           35           40           45
Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
           50           55           60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
           65           70           75           80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
           85           90           95
Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
           100           105           110
Glu Gly Cys Gly Cys Arg
           115

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
 1           5           10           15
Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
           20           25           30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
           35           40           45
Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
           50           55           60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
           65           70           75           80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
           85           90           95
Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
           100           105           110
Glu Gly Cys Gly Cys Arg

```

115

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vgr-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser	Arg	Gly	Ser	Gly	Ser	Ser	Asp	Tyr	Asn	Gly	Ser	Glu	Leu	Lys	Thr	1	5	10	15
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	20	25	30	
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	35	40	45	
Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	50	55	60	
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro	65	70	75	80
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	85	90	95	
Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	100	105	110	
Val	Arg	Ala	Cys	Gly	Cys	His										115			

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln	1	5	10	15
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	20	25	30	
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu				

		35				40				45									
Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His				
	50					55					60								
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro				
65					70				75					80					
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr				
			85					90					95						
Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val				
			100				105						110						
Val	Arg	Ala	Cys	Gly	Cys	His													
			115																

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BMP-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser	Arg	Met	Ser	Ser	Val	Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln				
1				5					10					15					
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp				
			20				25					30							
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp				
		35				40				45									
Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His				
	50					55					60								
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro				
65				70					75					80					
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr				
			85					90					95						
Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val				
			100				105						110						
Val	Arg	Ser	Cys	Gly	Cys	His													
			115																

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
 1             5             10             15
Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
          20             25             30
Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
          35             40             45
Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
          50             55             60
Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
          65             70             75             80
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
          85             90             95
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
          100            105            110
Thr Val Glu Ser Cys Ala Cys Arg
          115            120

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: MIS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
 1             5             10             15
Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
          20             25             30
Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
          35             40             45
Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
          50             55             60
Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
          65             70             75             80
Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
          85             90             95
Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
          100            105            110
Cys Gly Cys Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala
 1             5             10             15
Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp
      20             25             30
Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His
      35             40             45
Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro
      50             55             60
Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala
      65             70             75             80
Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val
      85             90             95
Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro
      100            105            110
Asn Leu Leu Thr Gln His Cys Ala Cys Ile
      115            120

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile
 1             5             10             15
Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
      20             25             30
Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
      35             40             45
Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
      50             55             60

```

His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe
65					70					75					80
Ala	Asn	Leu	Lys	Ser	Cys	Cys	Val	Pro	Thr	Lys	Leu	Arg	Pro	Met	Ser
				85					90					95	
Met	Leu	Tyr	Tyr	Asp	Asp	Gly	Gln	Asn	Ile	Ile	Lys	Lys	Asp	Ile	Gln
			100					105					110		
Asn	Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ser						
		115					120								

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His	Arg	Ile	Arg	Lys	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Arg	Thr	Asn	Leu
1				5					10					15	
Cys	Cys	Arg	Gln	Gln	Phe	Phe	Ile	Asp	Phe	Arg	Leu	Ile	Gly	Trp	Asn
			20					25					30		
Asp	Trp	Ile	Ile	Ala	Pro	Thr	Gly	Tyr	Tyr	Gly	Asn	Tyr	Cys	Glu	Gly
		35					40					45			
Ser	Cys	Pro	Ala	Tyr	Leu	Ala	Gly	Val	Pro	Gly	Ser	Ala	Ser	Ser	Phe
	50					55					60				
His	Thr	Ala	Val	Val	Asn	Gln	Tyr	Arg	Met	Arg	Gly	Leu	Asn	Pro	Gly
65					70					75					80
Thr	Val	Asn	Ser	Cys	Cys	Ile	Pro	Thr	Lys	Leu	Ser	Thr	Met	Ser	Met
				85					90					95	
Leu	Tyr	Phe	Asp	Asp	Glu	Tyr	Asn	Ile	Val	Lys	Arg	Asp	Val	Pro	Asn
			100					105					110		
Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ala							
		115					120								

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 1             5             10             15
Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
      20             25             30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
      35             40             45
Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
      50             55             60
Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
      65             70             75             80
Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
      85             90             95
Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
      100             105             110
Lys Cys Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
 1             5             10             15
Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
      20             25             30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
      35             40             45
Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
      50             55             60
Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
      65             70             75             80
Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
      85             90             95
Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
      100             105             110
Lys Cys Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: TGF-beta-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

[illegible]